

1/9

DD4b5.3 Coding Sequence

Length 2563 bp

GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCTGGTTCTTGTGGCCACCGTCGCT
1 R G Q V G A R S C C F W F S C G H R R C - 60
GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA
61 P A A L G C R T D K A W A T A P Q K P T - 120
CGCAGCTCGACGCAGGGGCGGCGAGGGGTGGGCGATCGCGTGTGAGGGGCGCCGCGC
121 Q L D A G A G R R V G D R V S E G A A R - 180
GGGCAGGCGGGCGGGCGCCAGAGGGGAAAGAGGCGGGGCGGGTCAAGCCGCTGGCC
181 A G G R A P E G E R G G G G G S A A G R - 240
GGGCCGGCGGGGAATGTCGATGCCTGACGCGATGCCGCTGCCCGGGTTCGGGGAGGAGC
241 A G G G M S M P D A M P L P G V G E E L - 300
TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCTTCATGGCCACCGTCACCA
301 K Q A K E I E D A E K Y S F M A T V T K - 360
AGGCGCCCAAGAAGCAAATCCAGTTTGTGATGACATGCAGGAGTTCACCAAATTCCCCA
361 A P K K Q I Q F A D D M Q E F T K F P T - 420
CCAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCTCCACTGACAGCTACA
421 K T G R R S L S R S I S Q S S T D S Y S - 480
GTTGAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC
481 S A A S Y T D S S D D E V S P R E K Q Q - 540
AAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAATCAAGCAGGCAGAATTTG
541 T N S K G S S N F C V K N I K Q A E F G - 600
GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC
601 R R E I E I A E Q D M S A L I S L R K R - 660
GTGCTCAGGGGGAGAAGCCCTTGGCTGGTGTCTAAATAGTGGGCTGTACACACATCACAG
661 A Q G E K P L A G A K I V G C T H I T A - 720
CCCAGACAGCGGTGTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTG
721 Q T A V L I E T L C A L G A Q C R W S A - 780
CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTG
781 C N I Y S T Q N E V A A A L A E A G V A - 840
CAGTGTTCGCTTGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTG
841 V F A W K G E S E D D F W W C I D R C V - 900
TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT
901 N M D G W Q A N M I L D D G G D L T H W - 960

FIG. 1

2/9

GGGTTTATAAGAAGTATCCAAACGTGTTTAAAGAAGATCCGAGGCATTGTGGAAGAGAGCG
961 -----+-----+-----+-----+-----+ 1020
V Y K K Y P N V F K K I R G I V E E S V -
TGACTGGTGTTCACAGGCTGTATCAGTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA
1021 -----+-----+-----+-----+-----+ 1080
T G V H R L Y Q L S K A G K L C V P A M -
TGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTGTACTGCTGCCGAGAAT
1081 -----+-----+-----+-----+-----+ 1140
N V N D S V T K Q K F D N L Y C C R E S -
CCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGG
1141 -----+-----+-----+-----+-----+ 1200
I L D G L K R T T D V M F G G K Q V V V -
TGTGTGGCTATGGTGAGGTAGGCAAGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAA
1201 -----+-----+-----+-----+-----+ 1260
C G Y G E V G K G C C A A L K A L G A I -
TTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCA
1261 -----+-----+-----+-----+-----+ 1320
V Y I T E I D P I C A L Q A C M D G F R -
GGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTGCACAGGAA
1321 -----+-----+-----+-----+-----+ 1380
V V K L N E V I R Q V D V V I T C T G N -
ATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCA
1381 -----+-----+-----+-----+-----+ 1440
K N V V T R E H L D R M K N S C I V C N -
ATATGGGGCACTCCAAACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGT
1441 -----+-----+-----+-----+-----+ 1500
M G H S N T E I D V T S L R T P E L T W -
GGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCC
1501 -----+-----+-----+-----+-----+ 1560
E R V R S Q V D H V I W P D G K R V V L -
TCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCACCTTTGTTCTGT
1561 -----+-----+-----+-----+-----+ 1620
L A E G R L L N L S C S T V P T F V L S -
CCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGC
1621 -----+-----+-----+-----+-----+ 1680
I T A T T Q A L A L I E L Y N A P E G R -
GATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGC
1681 -----+-----+-----+-----+-----+ 1740
Y K Q D V Y L L P K K M D E Y V A S L H -
ATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGG
1741 -----+-----+-----+-----+-----+ 1800
L P S F D A H L T E L T D D Q A K Y L G -
GACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATACTAATGGACCATACTAC
1801 -----+-----+-----+-----+-----+ 1860
L N K N G P F K P N Y Y R Y *
CAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTAAAGATAACTTTAT
1861 -----+-----+-----+-----+-----+ 1920
TTTCTTCTTACTGCTTTCGCTTTGATTTTTTTCCTATAATTCATTCTTGTTTTTTCATC
1921 -----+-----+-----+-----+-----+ 1980
TCATTATCCAAGTTCTGCAGACCACACAGGAACCTTGCTTCATGGCTCTTTAGATGAAATA
1981 -----+-----+-----+-----+-----+ 2040

FIG 1 (cont)

3/9

GAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCCCCAGCCCAGAAA
2041 -----+-----+-----+-----+-----+-----+ 2100
GGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGGTACCTTATTAACA
2101 -----+-----+-----+-----+-----+-----+ 2160
GGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGA
2161 -----+-----+-----+-----+-----+-----+ 2220
GCCCATTTCCTTAGCTGCTGAAATCAGTGCTCTTTCACCTCTTCAGAGAAGCAGGGATGGT
2221 -----+-----+-----+-----+-----+-----+ 2280
ACCTACCCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCA
2281 -----+-----+-----+-----+-----+-----+ 2340
AGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGG
2341 -----+-----+-----+-----+-----+-----+ 2400
CTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCCACCA
2401 -----+-----+-----+-----+-----+-----+ 2460
GACTTGCTCATTTTTCGAGTTTTTAAGTACTACACTCTATTTGAGTTTAATTTGTCC
2461 -----+-----+-----+-----+-----+-----+ 2520
TCTAGGATTTATTTCTGTTGTCCAAAAAAAAAAAAAAAAAAAAA
2521 -----+-----+-----+-----+-----+-----+ 2563

FIG 1 (Cont)

T04T30" F0029460

FIG 2

Alignment of DD4b5.3 AHCY-like domain with full-length AHCY amino acid sequences of human (hu), mouse (mu) and drosophila (dr).
Noted are conserved features shown to be important for AHCY function.



FIG 2

5/9

DD4b5.3 sequenc sch matic

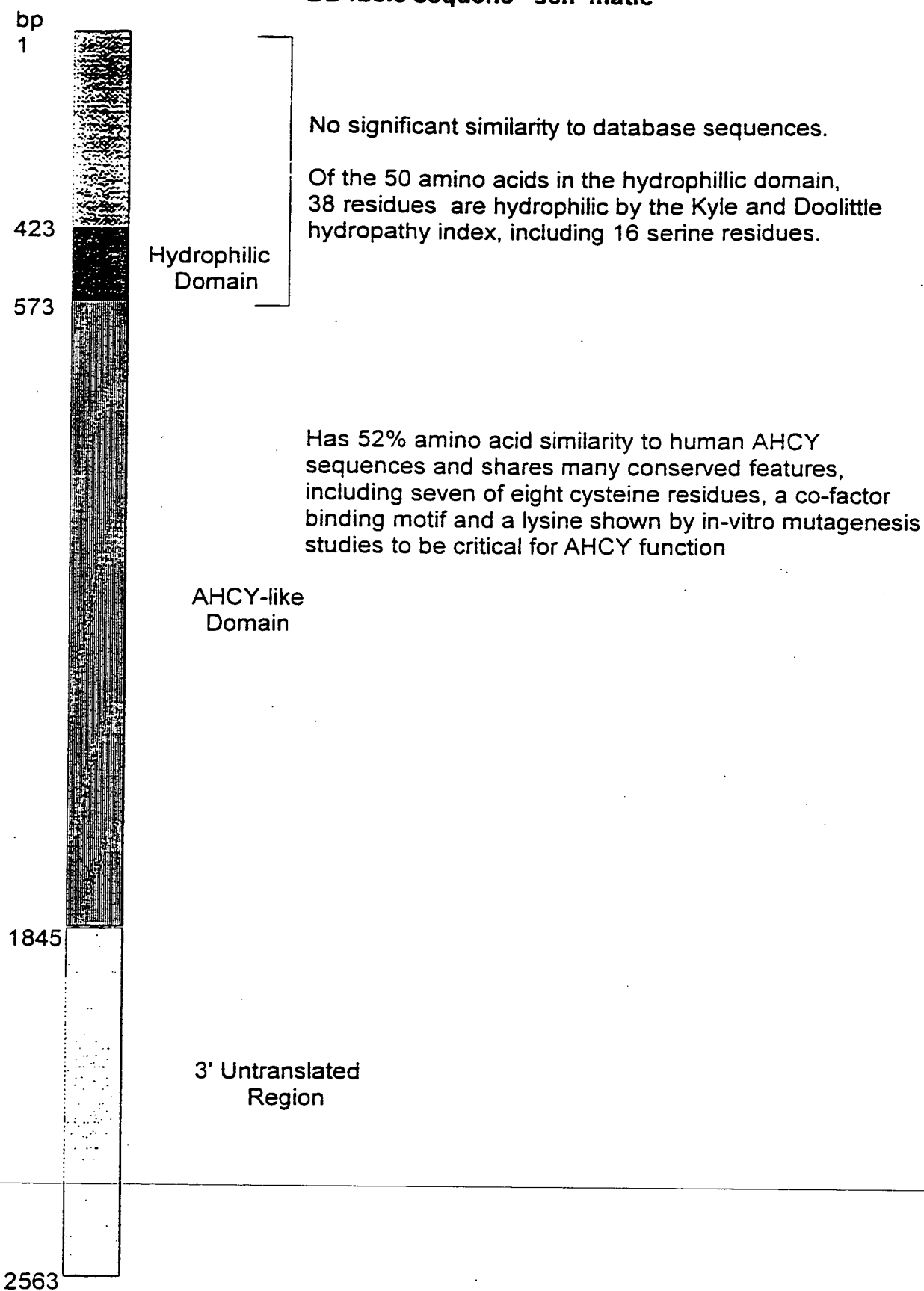
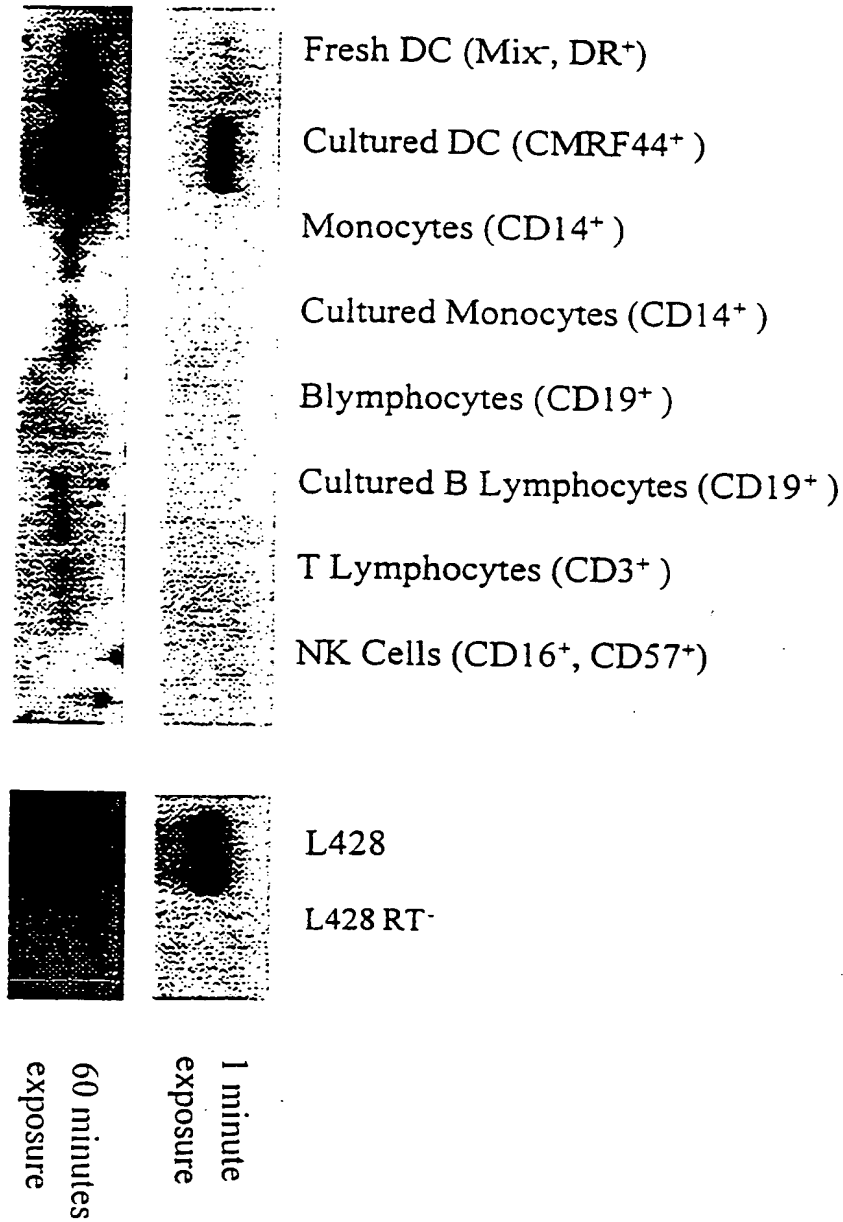


FIG 3

09700051.024401



Southern blot analysis of DD4b5.3 RT-PCR results

FIG 4

7/9

Expression of DD4b5.3 in DC lineage panel, as assessed by RT-PCR

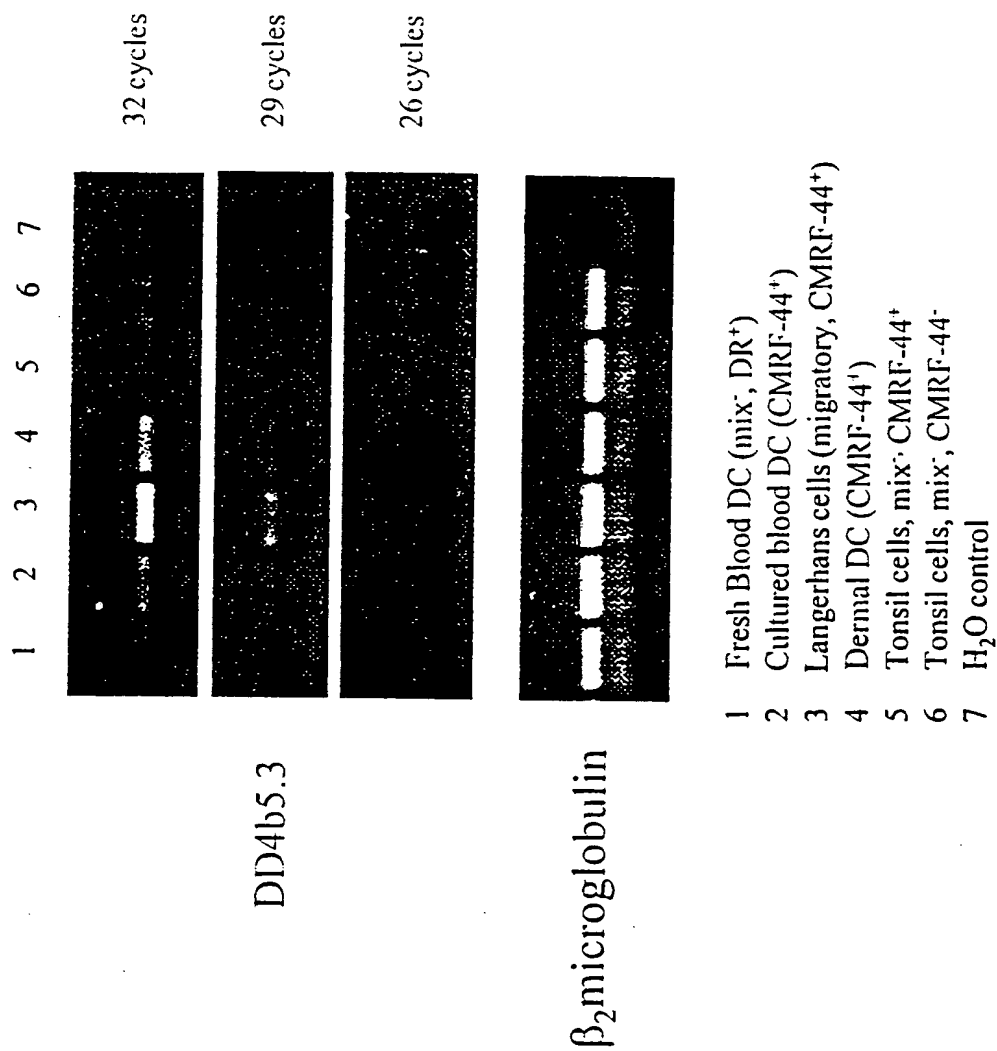


FIG 5

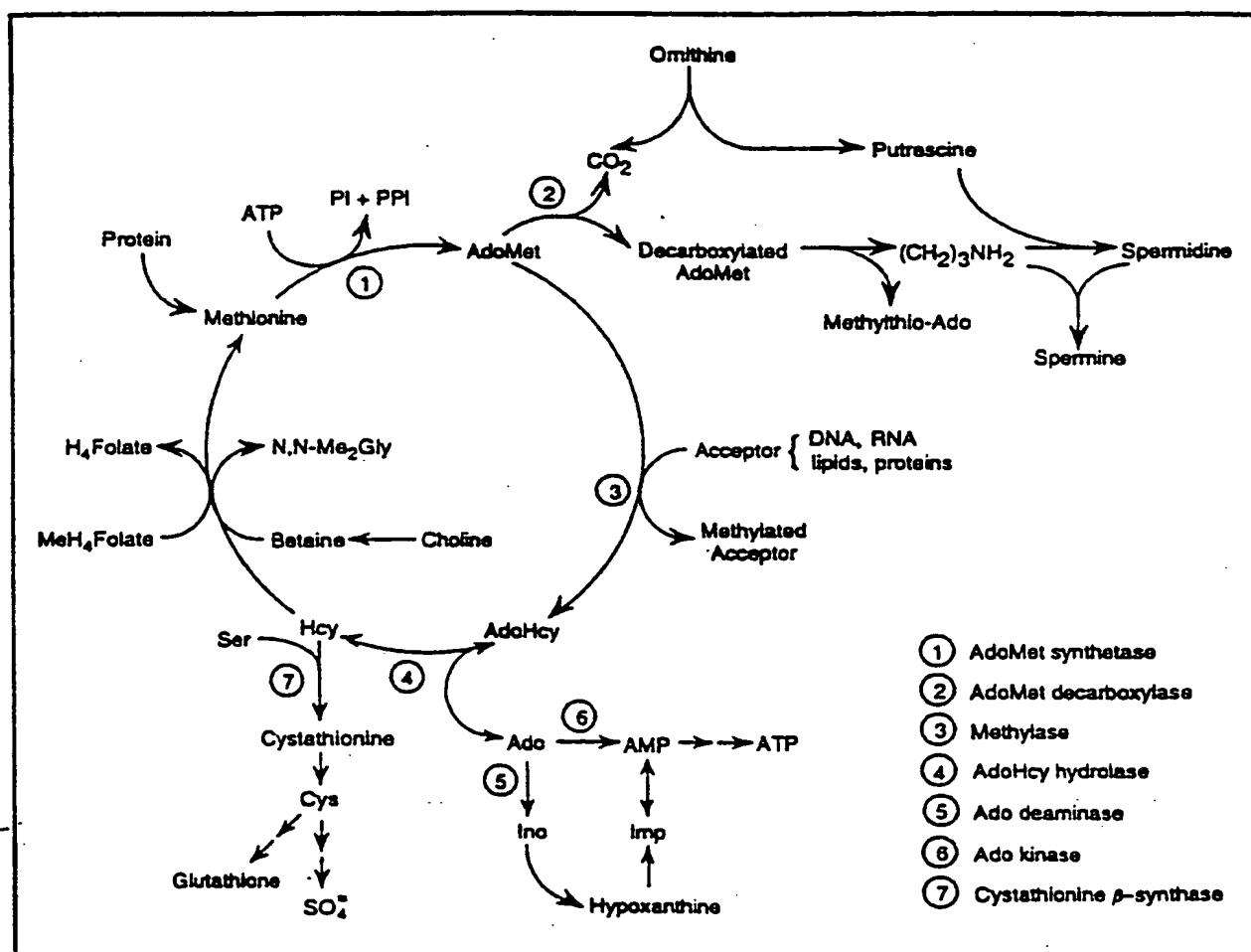


FIG 6

RAP-PCR Method

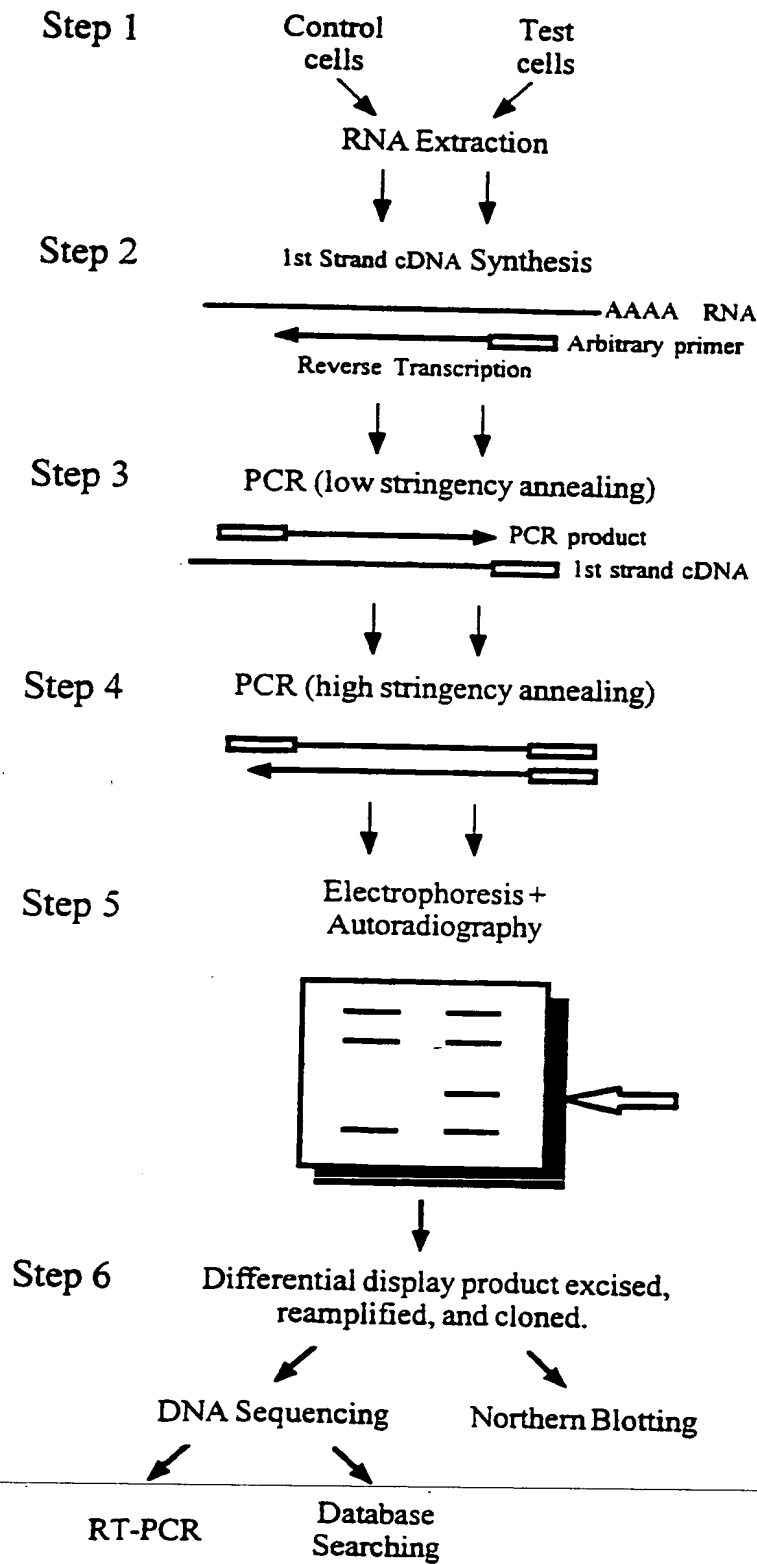


FIG 7